



UNITED STATES PATENT AND TRADEMARK OFFICE

ST

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/627,141	07/25/2003	Juan Carlos de la Torre	TSRI 465.0 D2	4125

26621 7590 02/06/2006

THE SCRIPPS RESEARCH INSTITUTE
OFFICE OF PATENT COUNSEL, TPC-8
10550 NORTH TORREY PINES ROAD
LA JOLLA, CA 92037

EXAMINER

CHEN, STACY BROWN

ART UNIT PAPER NUMBER

1648

DATE MAILED: 02/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/627,141

Applicant(s)

DE LA TORRE, JUAN CARLOS

Examiner

Stacy B. Chen

Art Unit

1648

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 17 November 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 5-59 is/are pending in the application.
- 4a) Of the above claim(s) 5-11, 16-27, 31-33 and 35-59 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 12, 28-30 and 34 is/are rejected.
- 7) ☒ Claim(s) 13-15 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 20 January 2004 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>11/17/04</u> . | 6) <input checked="" type="checkbox"/> Other: <u>Sequence Alignments</u> . |

DETAILED ACTION

1. Applicant's amendment filed November 17, 2005 is acknowledged. Claims 5-59 are pending. Claims 5-11, 16-27, 31-33 and 35-59 remain withdrawn from consideration being drawn to non-elected inventions. Claims 12-15, 28-30 and 34 remain under examination. Claim 34 is examined only with respect to the elected subject matter relating to claim 29, from which claim 34 depends. The other embodiments of claim 34 are not under examination.

In the previous Office action, the examiner indicated that SEQ ID NO: 28, 29, 30, 39, 40, 41, 13, 14 and 15 are free of the prior art of record. Upon further consideration and a careful review of the search results, SEQ ID NO: 40 is the only sequence that is free of the prior art of record. On January 20, 2005, the examiner and Michael McCarthy attempted to reach agreement on the claims in view of the examiner's new findings. In the interest of clarifying the record, this Office action is set forth. The examiner regrets any inconvenience to Applicant. In view of the new grounds of rejection, this action is made non-final.

2. A copy of the information disclosure statement PTO-1449 filed October 4, 2004 has been filed on November 17, 2005. The references have been considered, see attached PTO-1449.

Response to Arguments and Amendments

3. The following objection and rejections are withdrawn:

- The objection to claims 12-15 for minor informalities is withdrawn in view of Applicant's amendment.

Art Unit: 1648

- The rejection of claims 12-15, 28-30 and 34 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention, is withdrawn in view of Applicant's amendment.
- The rejection of claims 12-15, 28-30 and 34 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 7 of U.S. Patent No. 6,057,094, is withdrawn in view of Applicant's filing of a terminal disclaimer over the patented claim(s). The terminal disclaimer is acknowledged and accepted.

Claim Rejections - 35 USC § 112

4. (New Rejection) Claim 34 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 34 is drawn to a host cell. It is unclear whether the host cell is being referred to *in vitro* or *in vivo*. Suggested language is "An isolated host cell". Correction is required to overcome this rejection.

Claim Rejections - 35 USC § 102

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Art Unit: 1648

(*New Rejection*) Claims 12, 28-30 and 34 are rejected under 35 U.S.C. 102(b) as being anticipated by Bode *et al.* (*Molecular Psychiatry*, 1996, 1:200-212, “Bode”). The claims are drawn to a substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence SEQ ID NO: 28, 29 or 30. The polynucleotides are in vectors which are in host cells. The Office considers “consisting essentially of” to be open claim language. The Office’s interpretation of the claimed invention is a polynucleotide having SEQ ID NO: 28, for example, wherein the polynucleotide has additional nucleotides that do not materially affect the function of SEQ ID NO: 28.

Bode discloses BDV p40 polypeptide sequences that are 190 amino acids in length and have 100% sequence identity to Applicant’s SEQ ID NO: 28, 29 and 30 (see attached Sequence Alignments). SEQ ID NO: 28-30 are all 189 amino acids in length. Bode discloses that the nucleic acid sequences of the p40 polypeptides were obtained and inserted (vector) into an oligodendroglia cell line for expression. (In order for a protein to be expressed, the nucleic acid must have a promoter.) Based on the understanding of “consisting essentially of”, Bode’s polynucleotides read on Applicant’s polynucleotides. The extra amino acid in Bode’s sequence is not expected to materially affect the function of the protein. Thus, the polynucleotide encoding Bode’s protein anticipates Applicant’s claimed polynucleotides.

6. (*New Rejection*) Claims 12, 28-30 and 34 are rejected under 35 U.S.C. 102(b) as being anticipated by WO 96/21021, “WIPO document”. The claims are drawn to a substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence SEQ ID NO: 39. The polynucleotides are in

Art Unit: 1648

vectors which are in host cells. The Office considers “consisting essentially of” to be open claim language.

Figure 2 of the WIPO document discloses a polypeptide sequence of 370 amino acids in length that has 100% sequence identity to Applicant’s SEQ ID NO: 39 (see attached Sequence Alignment). Also taught are polynucleotides encoding the polypeptides, wherein the polynucleotides are inserted into a vector and expressed in cells (page 21, lines 12-30). (In order for a protein to be expressed, the nucleic acid must have a promoter.) Based on the understanding of “consisting essentially of”, the polynucleotides of the WIPO document read on Applicant’s polynucleotides. The extra amino acids in the polypeptide sequence are not expected to materially affect the function of the p40 protein, lacking evidence to the contrary.

7. *(New Rejection)* Claim 12 is rejected under 35 U.S.C. 102(b) as being anticipated by Cubitt *et al.* (*Journal of Virology*, 1994, 68(3):1382-1396, “Cubitt”). The claims are drawn to a substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence SEQ ID NO: 41. The polynucleotides are in vectors which are in host cells. The Office considers “consisting essentially of” to be open claim language.

Cubitt discloses a polynucleotide sequence encoding a polypeptide sequence of 370 amino acids in length that has 100% sequence identity to Applicant’s SEQ ID NO: 41. SEQ ID NO: 41 is 19 amino acids in length. Based on the understanding of “consisting essentially of”, the polynucleotides Cubitt read on Applicant’s polynucleotides. The extra amino acids in the

Art Unit: 1648

polypeptide sequence are not expected to materially affect the function of the p40 protein encoded by SEQ ID NO: 41, lacking evidence to the contrary.

Conclusion

8. No claim is allowed. SEQ ID NO: 40 is free of the prior art of record. Claims 13-15 are objected to for depending from rejected claim 12.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stacy B. Chen whose telephone number is 571-272-0896. The examiner can normally be reached on M-F (7:00-4:30). If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James C. Housel can be reached on 571-272-0902. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.



Stacy B. Chen
February 3, 2006

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-28
Perfect score: 978
Sequence: 1 HVTSPSLVFLCILLIPIGLHNA.....TIKEYLACMDATILIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	190	2	Q65468_BDV
2	970	99.2	370	1	VP40_BDV
3	970	99.2	370	2	O10395_BDV
4	970	99.2	370	2	O10401_BDV
5	970	99.2	370	2	O5GL86_BDV
6	970	99.2	370	2	O5GL92_BDV
7	970	99.2	370	2	O5GL95_BDV
8	970	99.2	370	2	O5GLC8_BDV
9	970	99.2	370	2	O5GLD1_BDV
10	970	99.2	370	2	O8B829_BDV
11	970	99.2	370	2	O910H1_BDV
12	970	99.2	370	2	O91UL4_BDV
13	970	99.2	370	2	O91UL8_BDV
14	970	99.2	370	2	O774E9_BDV
15	969	99.1	190	2	O65470_BDV
16	969	99.1	370	2	O10398_BDV
17	966	98.8	370	2	O5GL98_BDV
18	964	98.6	370	2	O5GL50_BDV
19	964	98.6	370	2	O5GL62_BDV
20	964	98.6	370	2	O5GL71_BDV
21	964	98.6	370	2	O5GLB3_BDV
22	963	98.5	369	2	O9Q9V1_BDV
23	960	98.2	370	2	O10392_BDV
24	954	97.5	190	2	O65469_BDV
25	904	92.4	176	2	O77429_BDV
26	904	92.4	176	2	O77430_BDV
27	904	92.4	176	2	O77431_BDV
28	904	92.4	176	2	O77432_BDV
29	904	92.4	176	2	O77433_BDV
30	904	92.4	176	2	O77434_BDV
31	904	92.4	176	2	Q9W8R2_BDV

32	890	91.0	176	2	Q9WN17_BDV	Q9WN17	borna disease
33	778	79.6	152	2	O9QCJ2_BDV	O9QCJ2	borna disease
34	751	76.8	146	2	O12852_BDV	O12852	borna disease
35	751	76.8	146	2	O12853_BDV	O12853	borna disease
36	751	76.8	146	2	O12855_BDV	O12855	borna disease
37	751	76.8	146	2	O12856_BDV	O12856	borna disease
38	751	76.8	146	2	O12857_BDV	O12857	borna disease
39	751	76.8	146	2	O12858_BDV	O12858	borna disease
40	751	76.8	146	2	O12859_BDV	O12859	borna disease
41	751	76.8	146	2	O12860_BDV	O12860	borna disease
42	751	76.8	146	2	O12861_BDV	O12861	borna disease
43	751	76.8	146	2	O12862_BDV	O12862	borna disease
44	751	76.8	146	2	O12863_BDV	O12863	borna disease
45	751	76.8	146	2	O12864_BDV	O12864	borna disease

ALIGNMENTS

RESULT 1	Q65468_BDV	PRELIMINARY;	PRT;	190 AA.
ID	Q65468; BDV			
AC	Q65468;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DS	P40 (Fragment).			
OS	Borna disease virus (BDV).			
OC	Borna disease virus (BDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae; Bornavirus.			
RN	NCBI_Taxid=12455;			
RX	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=97233300; PubMed=9118344;			
RA	Bode L., Duerrwald R., Rantam F.A., Perszt R., Ludwig H.;			
RT	"First isolates of infectious human Borna disease virus from patients with mood disorders";			
RL	Mol. Psychiatry 11:200-212 (1996).			
DR	EMBL; U58594; AAB05242.1; -; Genomic RNA.			
DR	HSSP; Q01552; IN93.			
DR	InterPro; IPR009441; BDV_P40.			
DR	PANTHER; PTHR10207; BDV_P40; 1.			
FT	Pfam; PF06407; BDV_P40; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	190 AA; 20896 MW; 75FECAB81370BB9C CRC64;		
Query Match	100.0%; Score 978; DB 2; Length 190;			
Best Local Similarity	100.0%; Pred. No. 1.1e-86;			
Matches	189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 HVTSPSLVFLCILLIPIGLHNAFVHGVPRESYSTPVRREQTVVTKAFYGEKTTORDLT 60			
DB	1 HVTSPSLVFLCILLIPIGLHNAFVHGVPRESYSTPVRREQTVVTKAFYGEKTTORDLT 60			
QY	61 ELKISISFHCSCSLIGVITGSSSKIKAQAOIKRKFXTMAALNRPSSHGRTATLLQMTN 120			
DB	61 ELKISISFHCSCSLIGVITGSSSKIKAQAOIKRKFXTMAALNRPSSHGRTATLLQMTN 120			
QY	121 PHEALDWMNGQPMWVSFVLPLITTPESPGRKFMQIKLVASYAOMTYTTTIKEYLACGM 180			
DB	121 PHEALDWMNGQPMWVSFVLPLITTPESPGRKFMQIKLVASYAOMTYTTTIKEYLACGM 180			
QY	181 DATLTIPV 189			
DB	181 DATLTIPV 189			
RESULT 2	VP40_BDV	STANDARD;	PRT;	3 AA.
ID	VP40_BDV			
AC	O01552;			
DT	01-JUL-1993 (Rel. 26, Created)			

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-29
Perfect score: 974
Sequence: 1 HTVPSIVFLCLIPGLHAA.....TTIKYVLAECMDATLPIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	100.0	190	2	Q65469_BDV
2	960	98.6	190	2	Q65470_BDV
3	959	98.5	370	1	VP40_BDV
4	959	98.5	370	2	Q10395_BDV
5	959	98.5	370	2	Q10401_BDV
6	959	98.5	370	2	Q5GL86_BDV
7	959	98.5	370	2	Q5GL92_BDV
8	959	98.5	370	2	Q5GL95_BDV
9	959	98.5	370	2	Q5GL98_BDV
10	959	98.5	370	2	Q5GLD1_BDV
11	959	98.5	370	2	Q8B829_BDV
12	959	98.5	370	2	Q910H1_BDV
13	959	98.5	370	2	Q91UH4_BDV
14	959	98.5	370	2	Q91UH8_BDV
15	959	98.5	370	2	Q774E9_BDV
16	958	98.4	370	2	Q10398_BDV
17	955	98.0	370	2	Q5GL98_BDV
18	954	97.9	190	2	Q65468_BDV
19	953	97.8	370	2	Q5GL50_BDV
20	953	97.8	370	2	Q5GL62_BDV
21	953	97.8	370	2	Q5GL71_BDV
22	953	97.8	370	2	Q5GLB3_BDV
23	952	97.7	369	2	Q9Q9V1_BDV
24	949	97.4	370	2	Q10392_BDV
25	893	91.7	176	2	Q77A29_BDV
26	893	91.7	176	2	Q77A30_BDV
27	893	91.7	176	2	Q77A31_BDV
28	893	91.7	176	2	Q77A32_BDV
29	893	91.7	176	2	Q77A33_BDV
30	893	91.7	176	2	Q77A34_BDV
31	893	91.7	176	2	Q9W8R2_BDV

32	879	90.2	176	2	Q9W17_BDV	Q9W17_borna disea
33	767	78.7	152	2	Q9QCJ2_BDV	Q9QCJ2_borna disea
34	740	76.0	146	2	Q12852_BDV	Q12852_borna disea
35	740	76.0	146	2	Q12853_BDV	Q12853_borna disea
36	740	76.0	146	2	Q12855_BDV	Q12855_borna disea
37	740	76.0	146	2	Q12856_BDV	Q12856_borna disea
38	740	76.0	146	2	Q12857_BDV	Q12857_borna disea
39	740	76.0	146	2	Q12858_BDV	Q12858_borna disea
40	740	76.0	146	2	Q12859_BDV	Q12859_borna disea
41	740	76.0	146	2	Q12860_BDV	Q12860_borna disea
42	740	76.0	146	2	Q12861_BDV	Q12861_borna disea
43	740	76.0	146	2	Q12862_BDV	Q12862_borna disea
44	740	76.0	146	2	Q12863_BDV	Q12863_borna disea
45	740	76.0	146	2	Q12864_BDV	Q12864_borna disea

ALIGNMENTS

RESULT 1	ID	Q65469_BDV	PRELIMINARY;	PRT;	190 AA.
AC	Q65469;				
DT	01-NOV-1996	(Tremblrel. 01, Created)			
DT	01-NOV-1996	(Tremblrel. 01, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			
DE	P40 (Fragment).				
OS	Borna disease virus (BDV).				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;				
OC	Bornavirus.				
OX	NCBI_TaxID=12455;				
RN	[1]				
RP	NCBIOTIDE SEQUENCE.				
RX	MEDLINE=97233300; PubMed=918344;				
RA	Bode U., Duerrwald R., Rantam F.A., Petzert R., Ludwig H.;				
RT	"First isolates of infectious human Borna disease virus from patients				
RT	with mood disorders.";				
RL	Mol. Psychiatry 1:200-212 (1996).				
DR	EMBL; U56595; AB05243.1; -; Genomic_RNA.				
DR	HSSP; Q01552; 1A93.				
DR	InterPro; IPR009441; BDV_P40.				
DR	PANTHER; PTHR10207; BDV_P40; 1.				
DR	Pfam; PF06407; BDV_P40; 1.				
FT	NON_TER	1			
FT	NON_TER	1			
SO	SEQUENCE	190 AA;	20959 MW;	OB6CCCC12BA62683 CRC64;	
Query Match 100.0%; Score 974; DB 2; Length 190;					
Best Local Similarity 100.0%; Pred. No. 2.9e-84;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	HTVPSIVFLCLIPGLHAAFHVGCVPRSTYLPTRGEQTVKTAFFGEKTTORDLT	60		
DB	1	HTVPSIVFLCLIPGLHAAFHVGCVPRSTYLPTRGEQTVKTAFFGEKTTORDLT	60		
QY	61	ELETSISFHCCLILGVVSSSKIKAEAOIKRRTWMAAANRSHGSTATLLQWEN	120		
DB	61	ELETSISFHCCLILGVVSSSKIKAEAOIKRRTWMAAANRSHGSTATLLQWEN	120		
QY	121	PHEAIDINQPMWGSFVLSLITDFSPGKRFMDQIKLVASVQMTTYTIKRYLAECM	180		
DB	121	PHEAIDINQPMWGSFVLSLITDFSPGKRFMDQIKLVASVQMTTYTIKRYLAECM	180		
QY	181	DATLTIPV 189			
DB	181	DATLTIPV 189			
RESULT 2					
ID	Q65470_BDV	PRELIMINARY;	PRT;	180 AA.	
AC	Q65470;				
DT	01-NOV-1996	(Tremblrel. 01, Created)			

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 / Search time 113.339 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975

Sequence: 1 HTWPSLVFCLIPGLHAA.....TTIKYVLAECMDATLTIPV 189

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	190	2	065470_BDV
2	974	99.9	370	1	VP40_BDV
3	974	99.9	370	2	010355_BDV
4	974	99.9	370	2	010401_BDV
5	974	99.9	370	2	05GL86_BDV
6	974	99.9	370	2	05GL92_BDV
7	974	99.9	370	2	05GL95_BDV
8	974	99.9	370	2	05GL98_BDV
9	974	99.9	370	2	05GLD1_BDV
10	974	99.9	370	2	08B829_BDV
11	974	99.9	370	2	0910H1_BDV
12	974	99.9	370	2	091UD4_BDV
13	974	99.9	370	2	091UR8_BDV
14	974	99.9	370	2	077A29_BDV
15	973	99.8	370	2	010398_BDV
16	970	99.5	370	2	05GL98_BDV
17	969	99.4	190	2	065468_BDV
18	968	99.3	370	2	05GL50_BDV
19	968	99.3	370	2	05GL62_BDV
20	968	99.3	370	2	05GL71_BDV
21	968	99.3	370	2	05GLB3_BDV
22	967	99.2	369	2	0909V1_BDV
23	964	98.9	370	2	010392_BDV
24	960	98.5	370	2	065469_BDV
25	908	93.1	176	2	077A29_BDV
26	908	93.1	176	2	077A30_BDV
27	908	93.1	176	2	077A31_BDV
28	908	93.1	176	2	077A32_BDV
29	908	93.1	176	2	077A33_BDV
30	908	93.1	176	2	077A34_BDV
31	908	93.1	176	2	09W8R2_BDV

32	894	91.7	176	2	09W17_BDV	Q9W17 borna disease
33	782	80.2	152	2	090CJ2_BDV	Q90CJ2 borna disease
34	755	77.4	146	2	012852_BDV	012852 borna disease
35	755	77.4	146	2	012853_BDV	012853 borna disease
36	755	77.4	146	2	012855_BDV	012855 borna disease
37	755	77.4	146	2	012856_BDV	012856 borna disease
38	755	77.4	146	2	012857_BDV	012857 borna disease
39	755	77.4	146	2	012858_BDV	012858 borna disease
40	755	77.4	146	2	012859_BDV	012859 borna disease
41	755	77.4	146	2	012860_BDV	012860 borna disease
42	755	77.4	146	2	012861_BDV	012861 borna disease
43	755	77.4	146	2	012862_BDV	012862 borna disease
44	755	77.4	146	2	012863_BDV	012863 borna disease
45	755	77.4	146	2	012864_BDV	012864 borna disease

ALIGNMENTS

RESULT 1						
ID	065470_BDV	PRELIMINARY;	PRT;	190 AA.		
AC	065470;					
DT	01-NOV-1996 (TREMblrel. 01, Created)					
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)					
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)					
DS	P40 (Fragment).					
OS	Borna disease virus (BDV).					
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae; Bornavirus.					
OX	NCBI_TaxID=12455;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=97233300; PubMed=918344;					
RA	Bode L., Duerrwald R., Rantam F.A., Ferez R., Ludwig H.;					
RT	"First isolates of infectious human Borna disease virus from patients with mood disorders."					
RL	Mol. Psychiatry 1:200-212(1996).					
DR	EMBL; U58596; AAB05244.1; -; Genomic RNA.					
DR	HSSP; Q01552; IN93.					
DR	InterPro; IPR009441; BDV_P40.					
DR	PANTHER; PTHR10207; BDV_P40; 1.					
DR	Pfam; PF06407; BDV_P40; 1.					
FT	NON_TER					
FT	NON_TER					
FT	NON_TER					
SO	SEQUENCE					
Query Match						
Best Local Similarity 100.0%; Score 975; DB 2; Length 190;						
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	HTWPSLVFCLIPGLHAAFHVGVPRESYLSPTIRGEQTVKAKFYGEKTTORDLT	60			
DB	1	HTWPSLVFCLIPGLHAAFHVGVPRESYLSPTIRGEQTVKAKFYGEKTTORDLT	60			
QY	61	ELBISSTFSHCCSLIGVTVGSSSKIKAGABQIKKRTMMALNRPSSHGTTATLLQWEN	120			
DB	61	ELBISSTFSHCCSLIGVTVGSSSKIKAGABQIKKRTMMALNRPSSHGTTATLLQWEN	120			
QY	121	PHEAIDWINGQPMWGSFVLSLTITDFSPKKEFMDQIKLVASVQMTTYTTIKYVLAECM	180			
DB	121	PHEAIDWINGQPMWGSFVLSLTITDFSPKKEFMDQIKLVASVQMTTYTTIKYVLAECM	180			
QY	181	DATLTIPV 189				
DB	181	DATLTIPV 189				
RESULT 2						
ID	VP40_BDV	STANDARD;	PRT;	3 AA.		
AC	001552;					
DT	01-JUL-1993 (Rel. 26, Created)					

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 / Search time 11.9228 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95
Sequence: 1 MPKRLVDDADAMEDQD 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	2 AAM49061	AAM49061 Human Bor
2	95	100.0	370	2 AAR98617	AAR98617 Borna dis
3	83	87.4	18	8 ADS75684	ADS75684 Borna dis
4	48.5	51.1	8	ADS43695	ADS43695 Bacterial
5	48	50.5	345	9 AEB27254	AEB27254 Plasmid rad
6	48	50.5	736	8 ADY10076	ADY10076 Plant ful
7	48	50.5	736	8 ADX77084	ADX77084 Plant ful
8	48	50.5	1134	7 ADE61439	ADE61439 Human pro
9	48	50.5	1526	4 AAM79777	AAM79777 Human pro
10	48	50.5	1526	4 ABG06116	ABG06116 Novel hum
11	48	50.5	1526	4 ABG07289	ABG07289 Novel hum
12	48	50.5	1552	4 AAM78793	AAM78793 Human pro
13	48	50.5	1554	4 ABG07288	ABG07288 Novel hum
14	48	50.5	1584	4 ABG07290	ABG07290 Novel hum
15	48	50.5	1627	4 ABG06117	ABG06117 Novel hum
16	48	50.5	1881	2 AAY24025	AAY24025 Membrane-act
17	46	48.4	131	3 AAY66712	AAY66712 Membrane-
18	46	48.4	131	3 AAY57844	AAY57844 Human lep
19	46	48.4	131	3 AAB03730	AAB03730 OR-RGRP2
20	46	48.4	131	3 AAY94849	AAY94849 Human pro
21	46	48.4	131	4 AAU29127	AAU29127 Human pro
22	46	48.4	131	4 AAB88337	AAB88337 Human mem
23	46	48.4	131	4 AAB65235	AAB65235 Human pro
24	46	48.4	131	5 ABB89581	ABB89581 Human pol

25	46	48.4	131	5 ABB84894	ABB84894 Human PRO
26	46	48.4	131	5 ABB95500	ABB95500 Human ang
27	46	48.4	131	5 ABUS5803	ABUS5803 Human PRO
28	46	48.4	131	6 ABUS8051	ABUS8051 Novel hum
29	46	48.4	131	6 ABUS84366	ABUS84366 Human sec
30	46	48.4	131	6 ABUS86240	ABUS86240 Human sec
31	46	48.4	131	6 ABUS86530	ABUS86530 Human sec
32	46	48.4	131	6 ABUS95570	ABUS95570 Human sec
33	46	48.4	131	6 ABUS8050	ABUS8050 Human PRO
34	46	48.4	131	6 ABUS9128	ABUS9128 Novel hum
35	46	48.4	131	6 ABUS82640	ABUS82640 Human sec
36	46	48.4	131	6 ABUS82809	ABUS82809 Human PRO
37	46	48.4	131	6 ABUS89930	ABUS89930 Novel hum
38	46	48.4	131	6 ABUS68179	ABUS68179 Human sec
39	46	48.4	131	6 ABUS60559	ABUS60559 Human sec
40	46	48.4	131	6 ABUS96232	ABUS96232 Novel hum
41	46	48.4	131	6 ABUS92663	ABUS92663 Human sec
42	46	48.4	131	6 ABUS08740	ABUS08740 Human sec
43	46	48.4	131	6 ABUS02792	ABUS02792 Human sec
44	46	48.4	131	6 ABUS74946	ABUS74946 Human sec
45	46	48.4	131	6 ABUS94708	ABUS94708 Human sec

ALIGNMENTS

RESULT 1
AAM49061 standard; peptide, 18 AA.

AC AAM49061;
AC 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
XX
XX Human Borna disease virus p40 peptide.
XX
XX BDV; infection; diagnosis; neuropsychiatric disorder; human.
XX
XX Borna disease virus.
OS
OS W09830238-A1.
XX
XX 16-JUL-1998.
XX
XX 07-JAN-1998; 98WO-US000495.
XX
XX 07-JAN-1997; 97US-00779764.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX De La Torre JC;
XX
XX WPI; 1998-398802/34.
XX
XX New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.
XX
XX Claim 5; Page 165; 207pp; English.

This peptide is characteristic of novel p40 proteins (see AAM49051-53) of human Borna disease virus (BDV) isolates obtained from psychiatric patients. The invention provides nucleic acids (see AAY2840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain poly:peptides (see AAM49043-63) obtained from psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV poly:peptides. Human BDV poly:peptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 AA;
SQ

Query Match 100.0%; Score 95; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPKRLVDDADAMEDOD 18
DB 1 MPKRLVDDADAMEDOD 18

RESULT 2
AAR98617 standard; protein; 370 AA.

XX AAR98617;
AC 16-OCT-2003 (revised)
DT 10-DEC-1996 (first entry)
XX
DE Borna disease virus p40.
XX
KM Borna disease virus; BDV; p40; nervous system disease;
KM neuro-psychiatric disease; schizophrenia; diagnosis; therapy; vaccine;
KM antibody.
XX
OS Borna disease virus; strain V.
XX
FN W09621020-A2.
XX
PD 11-JUL-1996.
XX
PF 05-JAN-1996; 96WO-US000418.
XX
PR 06-JAN-1995; 95US-00369822.
PR 04-MAY-1995; 95US-00434831.
PR 04-JAN-1996; 96US-00582776.
XX
PA (REGC) UNIV CALIFORNIA.

XX Lipkin W, Briese T, Kliche S, Schneider PA, Stitz L;
PI Schneemann A;
XX
DR WPI: 1996-333995/33.
DR N-PSDB; AAT38104.
XX
PT Borna disease virus (BDV) nucleotide and protein sequences - useful for
PT the diagnosis and treatment of infection and non-BDV related neuro-logic
PT and neuro-psychiatric disease.
XX
PS Disclosure; Fig 2; 186pp; English.
XX
CC Borna disease virus (BDV) p40 (AAR98617) was identified from an ORF on
CC the virus antigenome strand (AAT38104). p40 is expressed at high levels
CC in vitro and in vivo and is found in the nucleus and cytoplasm of BDV-
CC infected cells. Recombinant p40 was obtd. by PCR amplification (see also
CC AAT38113) of the p40 coding sequence and expression in Escherichia coli
CC transformants. It was used with BDV p23 (AAR98618) and gp18 (AAR98603) in
CC an ELISA for the detection of BDV antibodies. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX

XX Sequence 370 AA;

Query Match 100.0%; Score 95; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPKRLVDDADAMEDOD 18
DB 1 MPKRLVDDADAMEDOD 18

RESULT 3
AD575684 standard; peptide; 18 AA.

XX AD575684;
AC AD575684;
XX
DT 02-DEC-2004 (first entry)

DE Borna disease virus p40 protein fragment #1 for detecting BDV infections.
XX
KM detection; exogenous antigen; class switching; IgM; IgG; immunoglobulin;
KM BDV; Borna disease virus; p24.
XX
XX Borna disease virus.

XX EPI460426-A1.
XX
FN 22-SEP-2004.
XX
PD 19-MAR-2004; 2004BP-00006699.
XX
PF 20-MAR-2003; 2003JP-00078898.
PR 26-MAR-2003; 2003JP-00086490.
PR 26-MAR-2003; 2003JP-00086491.
XX
XX (SYSM-) SYSMEX CORP.

XX Yamauchi K, Horii Y, Takahama Y, Nagai S;
XX
DR WPI: 2004-679696/67.
XX

PT Detecting antibody against exogenous antigen e.g. Borna disease virus
PT (BDV), involves detecting the IgM antibody to the exogenous antigen.

XX Claim 14; SEQ ID NO 3; 33pp; English.

XX The invention relates to a method of detecting (M1) an antibody, where an
XX examination of a disease caused by an exogenous antigen is conducted, the
XX exogenous antigen being an antigen having a property in which the class
XX switching from the IgM antibody to the IgG antibody of immunoglobulin
XX antibodies raised against the antigen is achieved after two months
XX following the appearance of the IgM antibody, the method involves
XX detecting the IgM antibody to the exogenous antigen. The specification
XX also discloses a reagent (I) for detecting an anti-BDV antibody,
XX comprising an antigen polypeptide selected from the p10 region of a Borna
XX disease virus (BDV) protein. (M1) is useful for detecting an antibody
XX specific to an exogenous antigen. The exogenous antigen is a
XX microorganism, virus and/or proteinaceous substance, which may be the
XX cause of a disease of a human or of a mammal other than humans. The
XX exogenous antigen is preferably Borna disease virus (BDV). (I) is useful
XX for detecting anti-BDV antibody. (M1) is accurate and enables the
XX measurement of an antibody also in the early stage of the infection. (M1)
XX has high detection sensitivity. This sequence corresponds to a peptide
XX antigen from the BDV p40 protein and used in the method of the invention.

SQ Sequence 18 AA;

Query Match 87.4%; Score 83; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKRLVDDADAMEDOD 18
DB 1 PKRLVDDADAMEDOD 16

RESULT 4
ID ADS43695 standard; protein; 567 AA.

XX ADS43695;
AC ADS43695;
XX
DT 02-DEC-2004 (first entry)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 11.3939 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88

Sequence: 1 ELSEISAIIRMGIVTGLV 19

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	95.5	370	1 VP40_BDV	O01552 borna disease
2	84	95.5	370	2 Q774E9_BDV	Q774E9 borna disease
3	81	92.0	369	2 Q9Q9Y1_BDV	Q9Q9Y1 borna disease
4	81	92.0	370	2 O10392_BDV	O10392 borna disease
5	81	92.0	370	2 O10395_BDV	O10395 borna disease
6	81	92.0	370	2 O10401_BDV	O10401 borna disease
7	81	92.0	370	2 O5GL50_BDV	O5GL50 borna disease
8	81	92.0	370	2 O5GL62_BDV	O5GL62 borna disease
9	81	92.0	370	2 O5GL71_BDV	O5GL71 borna disease
10	81	92.0	370	2 O5GL92_BDV	O5GL92 borna disease
11	81	92.0	370	2 O5GL95_BDV	O5GL95 borna disease
12	81	92.0	370	2 O5GL98_BDV	O5GL98 borna disease
13	81	92.0	370	2 O5GLB3_BDV	O5GLB3 borna disease
14	81	92.0	370	2 O5GLC8_BDV	O5GLC8 borna disease
15	81	92.0	370	2 O5GLB29_BDV	O5GLB29 borna disease
16	81	92.0	370	2 Q910H1_BDV	Q910H1 borna disease
17	81	92.0	370	2 Q91U14_BDV	Q91U14 borna disease
18	81	92.0	370	2 Q91U18_BDV	Q91U18 borna disease
19	81	90.9	370	2 O10398_BDV	O10398 borna disease
20	80	90.9	370	2 O5GLA6_BDV	O5GLA6 borna disease
21	80	90.9	370	2 Q5GLD1_BDV	Q5GLD1 borna disease
22	48	54.5	123	2 Q8TM18_METAC	Q8TM18 methanobarc
23	48	54.5	256	2 Q9AME8_9POL	Q9AME8 elymus glau
24	48	54.5	358	2 Q5JDP0_PYRO	Q5JDP0 pyrococcus
25	47	53.4	188	2 O8ZYR2_PYRA	O8ZYR2 pyrobaculum
26	47	53.4	254	2 O81590_ANOMA	O81590 anomochloa
27	47	53.4	255	2 O81558_9POL	O81558 schizachyri
28	47	53.4	373	2 Q7N116_GLOV1	Q7N116 gloeobacter
29	46	52.3	90	2 Q513B4_MONAL	Q513B4 monoplectus
30	46	52.3	244	2 O81539_3POL	O81539 arundinella
31	46	52.3	244	2 O81539_3POL	O81539 arundinella

32	46	52.3	246	2 O81560_ZEATU	O81560 zea luxuria
33	46	52.3	247	2 O81596_METCU	O81596 melica cupa
34	46	52.3	248	2 O6UT05_3POL	O6UT05 elymus repe
35	46	52.3	249	2 O6UT02_TAECM	O6UT02 taeniatheru
36	46	52.3	249	2 O6UTU7_9POL	O6UTU7 elymus repe
37	46	52.3	249	2 O6UTU8_9POL	O6UTU8 elymus repe
38	46	52.3	249	2 O6UTV1_9POL	O6UTV1 elymus repe
39	46	52.3	249	2 O6UTV2_9POL	O6UTV2 elymus repe
40	46	52.3	249	2 O6UTV4_9POL	O6UTV4 elymus repe
41	46	52.3	249	2 O6UTV5_9POL	O6UTV5 elymus repe
42	46	52.3	249	2 O6UTV6_9POL	O6UTV6 elymus repe
43	46	52.3	249	2 O6UTV8_9POL	O6UTV8 elymus repe
44	46	52.3	249	2 O6UTW0_9POL	O6UTW0 elymus repe
45	46	52.3	249	2 O6UTW4_9POL	O6UTW4 elymus repe

ALIGNMENTS

RESULT 1
ID VP40_BDV STANDARD; PRT; 370 AA.
AC O01552;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 40 kDa protein.
GN Name=P40; Synonyms=P38;
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirinae.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C6;
RX MEDLINE=94149825; PubMed=7906311;
RA Cubitt B., Oldstone C., de la Torre J.C.;
RT "Sequence and genome organization of Borna disease virus";
RL J. Virol. 68:1382-1396(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=Clone B6;
RX MEDLINE=93303922; PubMed=8317098;
RA Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.B.;
RT "Genomic organization of the structural proteins of borna disease virus revealed by a cDNA clone encoding the 38-kDa protein";
RN Virology 195:229-238(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 10-370.
RC STRAIN=Gieszen / HE/80-3;
RA Binz T., Riehle H., Yamaaki J., Richt J.A., Grebenstein O., Rott R., Nienmann H.;
RT Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Halle BI/91;
RX MEDLINE=94076462; PubMed=8254777;
RA Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;
RT "Sequence conservation in field and experimental isolates of Borna disease virus";
RL J. Virol. 68:63-68(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V;
RX MEDLINE=94240137; PubMed=8183914;
RA Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H., Lipkin W.I.;
RT "Genomic organization of Borna disease virus";
RN Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).
RN [6]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=HR/80-1;
RX MEDLINE=93021385; PubMed=1404604;

RA McClure M.A., Thibault K.J., Hatalski C.G., Lipkin W.I.;
 RT "sequence similarity between Borna disease virus p40 and a duplicated
 RT domain within the paramyxovirus and rhabdovirus polymerase proteins";
 RL J. Virol. 66:6572-6577(1992).
 CC -1- FUNCTION: Could be involved in the transport of nucleoprotein
 CC particles from the nucleus to the cytoplasm.
 CC -1- SUBCELLULAR LOCATION: Nucleus and cytoplasm of the infected cells.
 CC CAUTION: It is uncertain whether Met-1 or Met-14 is the initiator.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L27077; AAA20663.1; -; Genomic_RNA.
 DR EMBL; S62821; AAB227261.1; ALT_INIT; Genomic_RNA.
 DR EMBL; X68392; CAA48458.1; ALT_INIT; mRNA.
 DR EMBL; S67502; AAB29214.1; -; Genomic_RNA.
 DR EMBL; U04608; AAA20224.1; -; Genomic_RNA.
 DR EMBL; M99375; AAA73385.1; ALT_INIT; mRNA.
 DR PDB; 1N93; X-ray; X=1-370.
 DR PDB; 1EP1; X-ray; X=1-370.
 DR InterPro; IPR009441; BDV_P40.
 DR PANTHER; PTHR10207; BDV_P40; 1.
 DR Pfam; PF06407; BDV_P40; 1.
 KM 3D-structure; Direct protein sequencing.
 FT VARIANT 47 47 I -> T (in strain HE/80-1).
 FT VARIANT 56 56 N -> S (in strain Halle BI/91).
 FT VARIANT 275 275 E -> D (in strain V).
 FT VARIANT 357 357 I -> V (in strain Halle BI/91).
 FT VARIANT 362 362 R -> K (in strain Halle BI/91 and strain
 FT V).
 FT CONFLICT 1 1 M -> L (in Ref. 6).
 SQ SEQUENCE 370 AA; 40981 MW; C02454BDABSE4B53 CRC64;
 Query Match 95.5%; Score 84; DB 1; Length 370;
 Best Local Similarity 100.0%; Pred. No. 5.8e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELSGEISAIWMIGVTGL 18
 DB 352 ELSGEISAIWMIGVTGL 369
 RESULT 2
 Q774E9 BDV PRELIMINARY; PRT; 370 AA.
 ID Q774E9 BDV PRELIMINARY; PRT; 370 AA.
 AC Q774E9;
 DT 10-MAY-2005 (TREMBLrel. 30. Created)
 DT 10-MAY-2005 (TREMBLrel. 30. Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30. Last annotation update)
 DE P40 protein (Nucleoprotein).
 OS Borna disease virus (BDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
 OC Bornavirus.
 OX NCBI_TaxID=12455;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CRP3A, CRP3B, and CRNP5;
 RX MEDLINE=22153693; PubMed=12163584;
 RX DOI=10.1128/JVI.76.17.8650-8658.2002;
 RA Nishino Y., Kobasa D., Rubin S.A., Pletnikov M.V., Carbone K.M.;
 RT "Enhanced neurovirulence of borna disease virus variants associated
 RT with nucleotide changes in the glycoprotein and L polymerase genes.";
 RL J. Virol. 76:8650-8658(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21488520; PubMed=11602780;
 RA Pleschka S., Staeheli P., Kolodziejek J., Richt J.A., Nowotny N.,
 RA Schwemmler M.;
 RT "Conservation of coding potential and terminal sequences in four
 RT different isolates of Borna disease virus.";

RL J. Gen. Virol. 82:2681-2690(2001).
 DR EMBL; AY114161; AAM68134.1; -; Genomic_RNA.
 DR EMBL; AY114162; AAM68140.1; -; Genomic_RNA.
 DR EMBL; AY114163; AAM68146.1; -; Genomic_RNA.
 DR EMBL; AJ311522; CAC70640.1; -; Genomic_RNA.
 KM Viral nucleoprotein.
 SQ SEQUENCE 370 AA; 40981 MW; C02454BDABSE4B53 CRC64;
 Query Match 95.5%; Score 84; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 5.8e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELSGEISAIWMIGVTGL 18
 DB 352 ELSGEISAIWMIGVTGL 369
 RESULT 3
 Q909V1 BDV PRELIMINARY; PRT; 369 AA.
 ID Q909V1 BDV PRELIMINARY; PRT; 369 AA.
 AC Q909V1;
 DT 01-MAY-2000 (TREMBLrel. 13. Created)
 DT 01-MAY-2000 (TREMBLrel. 13. Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 23. Last annotation update)
 DE N protein (Nucleoprotein).
 OS Borna disease virus (BDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
 OC Bornavirus.
 OX NCBI_TaxID=12455;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=No/98;
 RX MEDLINE=20283825; PubMed=10823873;
 RX DOI=10.1128/JVI.74.12.5655-5658.2000;
 RA Nowotny N., Kolodziejek J., Jehle C.O., Suchy A., Staeheli P.,
 RA Schwemmler M.;
 RT "Isolation and characterization of a new subtype of Borna disease
 RT virus.";
 RL J. Virol. 74:5655-5658(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=No/98;
 RX MEDLINE=21488520; PubMed=11602780;
 RA Pleschka S., Staeheli P., Kolodziejek J., Richt J.A., Nowotny N.,
 RA Schwemmler M.;
 RT "Conservation of coding potential and terminal sequences in four
 RT different isolates of Borna disease virus.";
 RL J. Gen. Virol. 82:2681-2690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=No/98;
 RX MEDLINE=21488520; PubMed=11602780;
 RA Nowotny N., Kolodziejek J., Jehle C.O., Suchy A., Staeheli P.,
 RA Schwemmler M.;
 RT "Isolation and characterization of a new subtype of Borna disease
 RT virus.";
 RL J. Gen. Virol. 82:2681-2690(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=No/98;
 RA Nowotny N., Kolodziejek J.;
 RT "Isolation and characterization of a new subtype of Borna disease
 RT virus.";
 RL J. Gen. Virol. 74:5655-5658(2000).
 DR EMBL; AF136236; AAF22169.1; -; Genomic_RNA.
 DR EMBL; AJ311524; CAC70654.1; -; Genomic_RNA.
 DR HSSP; Q01552; 1N93.
 DR InterPro; IPR009441; BDV_P40.
 DR PANTHER; PTHR10207; BDV_P40; 1.
 DR Pfam; PF06407; BDV_P40; 1.
 KM Viral nucleoprotein.
 SQ SEQUENCE 369 AA; 40930 MW; 9A5C9A95720F3BP9 CRC64;